

10/567764

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IAP5 Rec'd PCT/PTO 10 FEB 2006  
SEQUENCE LISTING

<110> Wyeth  
Flannery, Carl R  
Corcoran, Christopher J  
Freeman, Bethany A  
Racie, Lisa A

<120> RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

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Thr Thr Pro  
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&lt;223&gt; Translation of SEQ ID NO: 3.

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Glu	Thr	Ser	Leu	Thr 275	Val	Asn	Lys 280	Glu	Thr	Thr	Val	Glu	Thr	Lys	Glu 285
Thr	Thr	Thr	Thr	Asn	Lys	Gln 295	Thr	Ser	Thr	Asp	Gly 300	Lys	Glu	Lys	Thr
Thr	Ser	Ala	Lys	Glu	Thr	Gln 310	Ser	Ile	Glu	Lys 315	Thr	Ser	Ala	Lys	Asp 320
Leu	Ala	Pro	Thr	Ser 325	Lys	Val	Leu	Ala	Lys 330	Pro	Thr	Pro	Lys	Ala	Glu 335
Thr	Thr	Thr	Lys	Gly 340	Pro	Ala	Leu	Thr	Thr 345	Pro	Lys	Glu	Pro	Thr	Pro 350
Thr	Thr	Pro	Lys	Glu	Pro	Ala	Ser	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro 365
Thr	Thr	Ile	Lys	Ser	Ala	Pro 375	Thr	Thr	Pro	Lys	Glu 380	Pro	Ala	Pro	Thr
Thr	Thr	Lys	Ser	Ala	Pro 390	Thr	Thr	Pro	Lys	Glu 395	Pro	Ala	Pro	Thr	Thr 400
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu 410	Pro	Ala	Pro	Thr	Thr 415
Thr	Lys	Pro	Ala	Pro	Thr	Thr	Pro	Glu	Thr	Pro	Pro	Pro	Thr	Thr	Ser 430
Glu	Val	Ser	Thr	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Thr	Thr	Ile	His	Lys 445
Ser	Pro	Asp	Glu	Ser	Thr	Pro	Glu	Leu	Ser	Ala	Glu 460	Pro	Thr	Pro	Lys 455
Ala	Leu	Glu	Asn	Ser	Pro	Lys	Glu	Pro	Gly	Val 475	Pro	Thr	Thr	Lys	Thr 480
Pro	Ala	Ala	Thr	Lys 485	Pro	Glu	Met	Thr	Thr	Thr	Ala	Lys	Asp	Lys	Thr 495
Thr	Glu	Arg	Asp	Leu	Arg	Thr	Thr	Pro	Glu	Thr	Thr	Thr	Ala	Ala	Pro 510
Lys	Met	Thr	Lys	Glu	Thr	Ala	Thr	Thr	Thr	Glu	Lys	Thr	Thr	Glu	Ser 525

Lys Ile Thr Ala Thr Thr Thr Gln Val Thr Ser Thr Thr Thr Gln Asp  
 530 535 540  
 Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro  
 545 550 555 560  
 Lys Val Thr Thr Thr Lys Lys Thr Ile Thr Thr Thr Glu Ile Met Asn  
 565 570 575  
 Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys  
 580 585 590  
 Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro  
 595 600 605  
 Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg Val Arg Lys Pro Lys  
 610 615 620  
 Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr Met Pro Glu Leu Asn  
 625 630 635 640  
 Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln Thr Thr Thr Arg Pro  
 645 650 655  
 Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val Asn Pro Lys Ser Glu  
 660 665 670  
 Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His Met Leu Leu Arg Pro  
 675 680 685  
 His Val Phe Met Pro Glu Val Thr Pro Asp Met Asp Tyr Leu Pro Arg  
 690 695 700  
 Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met Leu Ser Asp Glu Thr  
 705 710 715 720  
 Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu Thr Thr Leu Arg Asn  
 725 730 735  
 Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe Trp Met Leu Ser Pro  
 740 745 750  
 Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr Glu Val Trp Gly Ile  
 755 760 765  
 Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys Asn Cys Glu Gly Lys  
 770 775 780  
 Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile  
 785 790 795 800  
 Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu  
 805 810 815  
 Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp  
 820 825 830  
 Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr  
 835 840 845

Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro Gly Arg Arg Pro Ala  
 850 855 860  
 Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln Val Arg Arg Arg Arg  
 865 870 875 880  
 Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln  
 885 890 895  
 Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn  
 900 905 910  
 Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr  
 915 920 925  
 Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr  
 930 935 940  
 Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg  
 945 950 955 960  
 Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val  
 965 970 975  
 Trp Tyr Asn Cys Pro  
 980

<210> 8  
 <211> 157  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8  
 gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc 60  
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaggagccag 120  
 ctctactac aacgaaaccg gcaccaacca ctccgga 157

<210> 9  
 <211> 51  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences between S373 to E425 in SEQ ID NO: 7).

<400> 9

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala  
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
                   20                  25                  30  
 Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro  
                   35                  40                  45  
 Thr Thr Pro  
             50

<210> 10  
 <211> 3024  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10  
 atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60  
 caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120  
 gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180  
 aagagagtct gcaactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240  
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300  
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360  
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420  
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480  
 tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540  
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600  
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660  
 gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cacgtctacc 720  
 acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780  
 agaccagtc ttccacctaa ttctgatata tctaaagaga cgtctttgac agtgaataaa 840  
 gagacaacag ttgaaactaa agaaactact acaacaata aacagacttc aactgatgga 900  
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960  
 ttagcaccca catctaaagt gctgggctaaa cctacacca aagctgaaac tacaaccaa 1020  
 ggccctgctc tcaccactcc caaggagccc acgcccacca ctccaagga gcctgcatct 1080  
 accacacca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140  
 cccgcaccta ccacgacaaa gtcagctcct actacgcca aagagccagc gccgacgact 1200

actaaagaac cggcaccac cagcctaataa gaaccagccc ctactacgac aaaggagcct	1260
gcaccacaaa ccacgaagag cgcaccacaca acaccaaagg agccggcccc tacgactcct	1320
aaggaaccca aaccggcacc aaccactccg gaaacacctc ctccaaccac ttcagaggtc	1380
tctactccaa ctaccaccaa ggagcctacc actatccaca aaagccctga tgaatcaact	1440
cctgagcttt ctgcagaacc cacacaaaaa gctcttgaaa acagtcccaa ggaacctggt	1500
gtacctacaa ctaagacgcc ggcggcgact aaacctgaaa tgactacaac agctaaagac	1560
aagacaacag aaagagactt acgtactaca cctgaaacta caactgctgc acctaatgatg	1620
acaaaagaga cagcaactac aacagaaaaa actaccgaat ccaaaataac agctacaacc	1680
acacaagtaa catctaccac aactcaagat accacaccat tcaaaattac tactcttaaa	1740
acaactactc ttgcacccaa agtaactaca acaaaaaaga caattactac cactgagatt	1800
atgaacaaac ctgaagaaac agctaaacca aaagacagag ctactaattc taaagcgaca	1860
actcctaaac ctcaaaagcc aaccaaagca cccaaaaaac ccacttctac caaaaagcca	1920
aaaacaatgc ctagagtgcg aaaaccaag acgacaccaa ctccccgcaa gatgacatca	1980
acaatgccag aattgaaccc tacctcaaga atagcagaag ccatgctcca aaccaccacc	2040
agacctaac aaactccaaa ctccaaacta gttgaagtaa atccaaagag tgaagatgca	2100
ggtggtgctg aaggagaaac acctcatatg cttctcaggc cccatgtgtt catgcctgaa	2160
gttactcccg acatggatta cttaccgaga gtacccaatc aaggcattat catcaatccc	2220
atgctttccg atgagaccaa tatatgcaat ggtaagccag tagatggact gactactttg	2280
cgcaatggga cattagtgc attccgaggt cattatttct ggatgctaag tccattcagt	2340
ccaccatctc cagctcgag aattactgaa gtttggggta ttccctcccc cattgatact	2400
gtttttacta ggtgcaactg tgaaggaaaa actttcttct ttaaggattc tcagtactgg	2460
cgtttttacca atgatataaa agatgcaggg taccacaaac caattttcaa aggatttgga	2520
ggactaactg gacaaatagt ggcagcgctt tcaacagcta aatataagaa ctggcctgaa	2580
tctgtgtatt ttttcaagag aggtggcagc attcagcagt atatttataa acaggaacct	2640
gtacagaagt gccctggaag aaggcctgct ctaaattatc cagtgtatgg agaaatgaca	2700
caggttagga gacgtcgctt tgaacgtgct ataggacctt ctcaaacaca caccatcaga	2760
attcaatatt cacctgccag actggcttat caagacaaag gtgtccttca taatgaagtt	2820
aaagtgagta tactgtggag aggacttcca aatgtgggta cctcagctat atcactgccc	2880
aacatcagaa aacctgacgg ctatgattac tatgcctttt ctaaagatca atactataac	2940
attgatgtgc ctagtagaac agcaagagca attactactc gttctgggca gaccttatcc	3000

aaagtctggt acaactgtcc ttaa

3024

&lt;210&gt; 11

&lt;211&gt; 1007

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Amino acid sequence of entire PRG4-LUB:2 protein.

&lt;400&gt; 11

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val  
 1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly  
 20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr  
 35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys  
 50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg  
 65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys  
 85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser  
 100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr  
 115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys  
 130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val  
 145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser  
 165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg  
 180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr  
 195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser  
 210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr  
 225 230 235 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys  
 245 250 255  
 Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys  
 260 265 270  
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu  
 275 280 285  
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr  
 290 295 300  
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp  
 305 310 315 320  
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu  
 325 330 335  
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro  
 340 345 350  
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro  
 355 360 365  
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr  
 370 375 380  
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 385 390 395 400  
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 405 410 415  
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro  
 420 425 430  
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr  
 435 440 445  
 Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr  
 450 455 460  
 Thr Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr  
 465 470 475 480  
 Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro  
 485 490 495  
 Lys Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro  
 500 505 510  
 Glu Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg  
 515 520 525  
 Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr  
 530 535 540  
 Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr  
 545 550 555 560



Thr Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile  
 565 570 575  
 Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys  
 580 585 590  
 Lys Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala  
 595 600 605  
 Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro  
 610 615 620  
 Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro  
 625 630 635 640  
 Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg  
 645 650 655  
 Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala  
 660 665 670  
 Glu Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser  
 675 680 685  
 Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu  
 690 695 700  
 Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu  
 705 710 715 720  
 Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile  
 725 730 735  
 Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys  
 740 745 750  
 Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe  
 755 760 765  
 Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro  
 770 775 780  
 Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr  
 785 790 795 800  
 Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp  
 805 810 815  
 Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro  
 820 825 830  
 Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala  
 835 840 845  
 Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe  
 850 855 860  
 Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro

18

865		870		875		880									
Val	Gln	Lys	Cys	Pro	Gly	Arg	Arg	Pro	Ala	Leu	Asn	Tyr	Pro	Val	Tyr
				885					890					895	
Gly	Glu	Met	Thr	Gln	Val	Arg	Arg	Arg	Arg	Phe	Glu	Arg	Ala	Ile	Gly
			900					905					910		
Pro	Ser	Gln	Thr	His	Thr	Ile	Arg	Ile	Gln	Tyr	Ser	Pro	Ala	Arg	Leu
		915					920					925			
Ala	Tyr	Gln	Asp	Lys	Gly	Val	Leu	His	Asn	Glu	Val	Lys	Val	Ser	Ile
	930					935					940				
Leu	Trp	Arg	Gly	Leu	Pro	Asn	Val	Val	Thr	Ser	Ala	Ile	Ser	Leu	Pro
945					950					955					960
Asn	Ile	Arg	Lys	Pro	Asp	Gly	Tyr	Asp	Tyr	Tyr	Ala	Phe	Ser	Lys	Asp
				965					970					975	
Gln	Tyr	Tyr	Asn	Ile	Asp	Val	Pro	Ser	Arg	Thr	Ala	Arg	Ala	Ile	Thr
			980					985					990		
Thr	Arg	Ser	Gly	Gln	Thr	Leu	Ser	Lys	Val	Trp	Tyr	Asn	Cys	Pro	
		995					1000					1005			

<210> 12  
 <211> 235  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic cDNA cassette-2 sequence.

<400> 12  
 gcgcgcccac aactccaaaa gagcccgacac ctaccacgac aaagtcagct cctactacgc 60  
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120  
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180  
 aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga 235

<210> 13  
 <211> 77  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences between S373 and E451 in SEQ ID NO: 11).

<400> 13

Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala
1				5				10					15		

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro  
 50 55 60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro  
 65 70 75

<210> 14  
 <211> 3117  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Recombinant PRG4-Lub:3 cDNA construct.

<400> 14  
 atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60  
 caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120  
 gatgccacct gcaactgtga ttataactgt caaactaca tggagtgctg ccttgatttc 180  
 aagagagtct gcaactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240  
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300  
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360  
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420  
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480  
 tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540  
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600  
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660  
 gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720  
 acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc 780  
 agaccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840  
 gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900  
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960  
 ttagcaccca catctaaagt gctggctaaa cctacacca aagctgaaac tacaaccaa 1020  
 ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140  
cccgcaccta ccacgacaaa gtcagctcct actacgcca aagagccagc gccgacgact 1200  
actaaagaac cggcaccac cagcctaata gaaccagccc ctactacgac aaaggagcct 1260  
gcaccacaaa ccacgaagag cgcaccacac acaccaaagg agccggcccc tacgactcct 1320  
aaagaaccag cccctactac gacaaaggag cctgcacca caaccacgaa gagcgacccc 1380  
acaacaccaa aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact 1440  
ccggaacac ctctccaac cacttcagag gtctctactc caactaccac caaggagcct 1500  
accactatcc aaaaaagccc tgatgaatca actcctgagc tttctgcaga acccacacca 1560  
aaagctcttg aaacagtc caaggaacct ggtgtaccta caactaagac gccggcgcg 1620  
actaaacctg aatgactac aacagctaaa gacaagacaa cagaaagaga cttacgtact 1680  
acacctgaaa ctacaactgc tgcacctaag atgacaaaag agacagcaac tacaacagaa 1740  
aaaactaccg aatccaaaat aacagctaca accacacaag taacatctac cacaactcaa 1800  
gataccacac cattcaaat tactactott aaaacaacta ctcttgacc caaagtaact 1860  
acaacaaaaa agacaattac taccactgag attatgaaca aacctgaaga aacagctaaa 1920  
ccaaaagaca gagctactaa ttctaaagcg acaactccta aacctcaaaa gccaaccaaa 1980  
gcacccaaaa aaccacttc taccaaaaag ccaaaaacaa tgcctagagt gagaaaacca 2040  
aagacgacac caactccccg caagatgaca tcaacaatgc cagaattgaa ccctacctca 2100  
agaatagcag aagccatgct ccaaaccacc accagaccta accaaactcc aaactccaaa 2160  
ctagttgaag taaatccaaa gagtgaagat gcaggtggtg ctgaaggaga aacacctcat 2220  
atgcttctca ggccccatgt gttcatgcct gaagtactc cgcacatgga ttacttaccg 2280  
agagtacca atcaaggcat tatcatcaat cccatgcttt ccgatgagac caatatatgc 2340  
aatggtaagc cagtagatgg actgactact ttgcgcaatg ggacattagt tgcattccga 2400  
ggtcattatt tctggatgct aagtccattc agtccaccat ctccagctcg cagaattact 2460  
gaagtttggg gtattccttc cccattgat actgttttta ctaggtgcaa ctgtgaagga 2520  
aaaactttct tctttaagga ttctcagtac tggcgtttta ccaatgatat aaaagatgca 2580  
gggtacccca aaccaatttt caaaggattt ggaggactaa ctggacaaat agtggcagcg 2640  
ctttcaacag ctaaataata gaactggcct gaatctgtgt attttttcaa gagaggtggc 2700  
agcattcagc agtatattta taaacaggaa cctgtacaga agtgccctgg aagaaggcct 2760  
gctctaaatt atccagtgt tggagaaatg acacaggtta ggagacgtcg ctttgaacgt 2820  
gctataggac cttctcaaac acacaccatc agaattcaat attcacctgc cagactggct 2880

tatcaagaca aaggtgtcct tcataatgaa gttaaagtga gtatactgtg gagaggactt 2940  
 ccaaagtgtg ttacctcagc tatatcactg cccaacatca gaaaacctga cggctatgat 3000  
 tactatgcct tttctaaaga tcaatactat aacattgatg tgcttagtag aacagcaaga 3060  
 gcaattacta ctcgttctgg gcagacctta tccaaagtct ggtacaactg tccttaa 3117

<210> 15

<211> 1038

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of entire PRG4-LUB:3 protein

<400> 15

Met	Ala	Trp	Lys	Thr	Leu	Pro	Ile	Tyr	Leu	Leu	Leu	Leu	Leu	Ser	Val	1	5	10	15
Phe	Val	Ile	Gln	Gln	Val	Ser	Ser	Gln	Asp	Leu	Ser	Ser	Cys	Ala	Gly	20	25	30	
Arg	Cys	Gly	Glu	Gly	Tyr	Ser	Arg	Asp	Ala	Thr	Cys	Asn	Cys	Asp	Tyr	35	40	45	
Asn	Cys	Gln	His	Tyr	Met	Glu	Cys	Cys	Pro	Asp	Phe	Lys	Arg	Val	Cys	50	55	60	
Thr	Ala	Glu	Leu	Ser	Cys	Lys	Gly	Arg	Cys	Phe	Glu	Ser	Phe	Glu	Arg	65	70	75	80
Gly	Arg	Glu	Cys	Asp	Cys	Asp	Ala	Gln	Cys	Lys	Lys	Tyr	Asp	Lys	Cys	85	90	95	
Cys	Pro	Asp	Tyr	Glu	Ser	Phe	Cys	Ala	Glu	Val	His	Asn	Pro	Thr	Ser	100	105	110	
Pro	Pro	Ser	Ser	Lys	Lys	Ala	Pro	Pro	Pro	Ser	Gly	Ala	Ser	Gln	Thr	115	120	125	
Ile	Lys	Ser	Thr	Thr	Lys	Arg	Ser	Pro	Lys	Pro	Pro	Asn	Lys	Lys	Lys	130	135	140	
Thr	Lys	Lys	Val	Ile	Glu	Ser	Glu	Glu	Ile	Thr	Glu	Glu	His	Ser	Val	145	150	155	160
Ser	Glu	Asn	Gln	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	165	170	175	
Ser	Thr	Ile	Trp	Lys	Ile	Lys	Ser	Ser	Lys	Asn	Ser	Ala	Ala	Asn	Arg	180	185	190	
Glu	Leu	Gln	Lys	Lys	Leu	Lys	Val	Lys	Asp	Asn	Lys	Lys	Asn	Arg	Thr	195	200	205	

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser  
 210 215 220  
 Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr  
 225 230 235 240  
 Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys  
 245 250 255  
 Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys  
 260 265 270  
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu  
 275 280 285  
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr  
 290 295 300  
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp  
 305 310 315 320  
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu  
 325 330 335  
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro  
 340 345 350  
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro  
 355 360 365  
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr  
 370 375 380  
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 385 390 395 400  
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 405 410 415  
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro  
 420 425 430  
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr  
 435 440 445  
 Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys  
 450 455 460  
 Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr  
 465 470 475 480  
 Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr  
 485 490 495  
 Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro  
 500 505 510  
 Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys  
 515 520 525

Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu  
 530 535 540  
 Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr  
 545 550 555 560  
 Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala  
 565 570 575  
 Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr  
 580 585 590  
 Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr  
 595 600 605  
 Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys  
 610 615 620  
 Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys  
 625 630 635 640  
 Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln  
 645 650 655  
 Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys  
 660 665 670  
 Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys  
 675 680 685  
 Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu  
 690 695 700  
 Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys  
 705 710 715 720  
 Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly  
 725 730 735  
 Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val  
 740 745 750  
 Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile  
 755 760 765  
 Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro  
 770 775 780  
 Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg  
 785 790 795 800  
 Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala  
 805 810 815  
 Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val  
 820 825 830  
 Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser

835	840	845
Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys 850 855 860		
Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala 865 870 875 880		
Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe 885 890 895		
Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val 900 905 910		
Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly 915 920 925		
Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro 930 935 940		
Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala 945 950 955 960		
Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu 965 970 975		
Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn 980 985 990		
Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp Gln 995 1000 1005		
Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr 1010 1015 1020		
Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro 1025 1030 1035		

&lt;210&gt; 16

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic cDNA cassette-2 sequences.

&lt;400&gt; 16

gcgcgccac aactcctaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240

ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaagg 300



aaccctaaacc ggcaccaacc actccgga

328

&lt;210&gt; 17

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences between S373 and E482 in SEQ ID NO: 15)

&lt;400&gt; 17

Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala
1				5					10					15	

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
			20					25					30		

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
			35				40					45			

Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro
	50					55					60				

Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala	Pro
65				70						75				80	

Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr
			85						90					95	

Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	Thr	Pro
			100					105			

&lt;210&gt; 18

&lt;211&gt; 3210

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; recombinant PRG4-Lub:4 cDNA construct.

&lt;400&gt; 18

atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag	60
caagtttcat ctcaagattt atcaagctgt gcaggagat gtggggaagg gtattctaga	120
gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtcg ccctgatttc	180
aagagagtct gcaactgcga gctttcctgt aaaggccgct gctttgagtc cttcgagaga	240
gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgtcg tcccgattat	300
gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct	360
ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca	420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt	480
tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg	540
aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta	600
aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat	660
gaagctggaa gtggattgga caatgggtgac ttcaagggtca caactcctga cacgtctacc	720
acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc	780
agaccagtc ttccaccta ttctgatata tctaaagaga cgtctttgac agtgaataaa	840
gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga	900
aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat	960
ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaa	1020
ggccctgctc tcaccactcc caaggagccc acgcccacca ctccaagga gcctgcatct	1080
accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag	1140
cccgaccta ccacgacaaa gtcagctcct actacgccc aagagccagc gccgacgact	1200
actaaagaac cggcacccac cagcctaaa gaaccagccc ctactacgac aaaggagcct	1260
gcaccacaaa ccacgaagag cgcaccacaa acaccaaagg agccggcccc tacgactcct	1320
aaagaaccag ccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc	1380
acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag	1440
gagcctgcac ccacaaccac gaagagcgca ccacaaacac caaaggagcc ggcccctacg	1500
actcctaagg aacccaaacc ggcaccaacc actccggaaa cacctcctcc aaccacttca	1560
gaggtctcta ctccaactac caccaaggag cctaccacta tccacaaaag ccctgatgaa	1620
tcaactcctg agctttctgc agaaccacaa ccaaaagctc ttgaaaacag tccaaggaa	1680
cctgggtgtac ctacaactaa gacgccggcg gcgactaaac ctgaaatgac tacaacagct	1740
aaagacaaga caacagaaag agacttacgt actacacctg aaactacaac tgctgcacct	1800
aagatgacaa aagagacagc aactacaaca gaaaaaacta ccgaatccaa aataacagct	1860
acaaccacac aagtaacatc taccacaact caagatacca caccattcaa aattactact	1920
cttaaaacaa ctactcttgc acccaaagta actacaacaa aaaagacaat tactaccact	1980
gagattatga acaaacctga agaaacagct aaacccaaaag acagagctac taattctaaa	2040
gcgacaactc ctaaacctca aaagccaacc aaagcaccca aaaaaccac ttctacaaa	2100
aagccaaaaa caatgcctag agtgagaaaa ccaagacga caccaactcc ccgcaagatg	2160
acatcaacaa tgccagaatt gaaccctacc tcaagaatag cagaagccat gctccaaacc	2220

accaccagac ctaaccaaac tccaaactcc aaactagttg aagtaaatecc aaagagtga 2280  
 gatgcagggtg gtgctgaagg agaaacacct catatgcttc tcaggcccca tgtgttcatg 2340  
 cctgaagtta ctcccgacat ggattactta ccgagagtac ccaatcaagg cattatcatc 2400  
 aatcccatgc tttccgatga gaccaatata tgcaatggta agccagtaga tggactgact 2460  
 actttgcgca atgggacatt agttgcattc cgagggtcatt atttctggat gctaagtcca 2520  
 ttcagtccac catctccagc tcgcagaatt actgaagttt ggggtattcc ttccccatt 2580  
 gatactgttt ttactaggtg caactgtgaa ggaaaaactt tcttctttaa ggattctcag 2640  
 tactggcggtt ttaccaatga tataaaagat gcagggtacc ccaaaccaat tttcaaagga 2700  
 tttggaggac taactggaca aatagtggca gcgctttcaa cagctaaata taagaactgg 2760  
 cctgaatctg tgtatTTTTT caagagaggt ggcagcattc agcagtatat ttataaacag 2820  
 gaacctgtac agaagtgcc tggaagaagg cctgctctaa attatccagt gtatggagaa 2880  
 atgacacagg ttaggagacg tcgctttgaa cgtgctatag gacottctca aacacacacc 2940  
 atcagaattc aatattcacc tgccagactg gcttatcaag acaaaggtgt ccttcataat 3000  
 gaagttaaag tgagtatact gtggagagga cttccaaatg tggttacctc agctatatca 3060  
 ctgccaaca tcagaaaacc tgacggctat gattactatg ctttttctaa agatcaatac 3120  
 tataacattg atgtgcctag tagaacagca agagcaatta ctactcggtc tgggcagacc 3180  
 ttatccaaag tctggtacaa ctgtccttaa 3210

<210> 19

<211> 1069

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val  
1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly  
20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr  
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys  
50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg

65		70		75		80
Gly Arg Glu Cys Asp	Cys Asp Ala Gln Cys Lys Lys Tyr Asp	Lys Cys				
85		90			95	
Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser		100	105		110	
Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr		115	120		125	
Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys		130	135		140	
Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val		145	150		155	160
Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser		165		170		175
Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg		180		185		190
Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr		195		200		205
Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser		210		215		220
Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr		225		230		235
Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys		245		250		255
Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys		260		265		270
Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu		275		280		285
Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr		290		295		300
Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp		305		310		315
Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu		325		330		335
Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro		340		345		350
Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro		355		360		365
Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr		370		375		380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 385 390 395 400  
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 405 410 415  
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro  
 420 425 430  
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr  
 435 440 445  
 Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys  
 450 455 460  
 Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys  
 465 470 475 480  
 Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu  
 485 490 495  
 Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro  
 500 505 510  
 Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr  
 515 520 525  
 Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu  
 530 535 540  
 Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu  
 545 550 555 560  
 Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met  
 565 570 575  
 Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr  
 580 585 590  
 Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr  
 595 600 605  
 Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln  
 610 615 620  
 Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr  
 625 630 635 640  
 Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr  
 645 650 655  
 Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro  
 660 665 670  
 Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys  
 675 680 685  
 Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr  
 690 695 700

Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met  
 705 710 715 720  
 Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala  
 725 730 735  
 Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu  
 740 745 750  
 Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu  
 755 760 765  
 Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr  
 770 775 780  
 Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile  
 785 790 795 800  
 Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val  
 805 810 815  
 Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly  
 820 825 830  
 His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg  
 835 840 845  
 Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe  
 850 855 860  
 Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln  
 865 870 875 880  
 Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro  
 885 890 895  
 Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu  
 900 905 910  
 Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys  
 915 920 925  
 Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln  
 930 935 940  
 Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu  
 945 950 955 960  
 Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser  
 965 970 975  
 Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr  
 980 985 990  
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp  
 995 1000 1005  
 Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn

1010	1015	1020
Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp		
1025	1030	1035
Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile		
1040	1045	1050
Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys		
1055	1060	1065

Pro

<210> 20  
 <211> 421  
 <212> DNA  
 <213> Artificial

<220>

<223> Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA cassette-2 sequences.

<400> 20  
 gcgcgcccac aactccaaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60  
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120  
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180  
 aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240  
 ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaaag 300  
 aaccagcccc tactacgaca aaggagcctg caccacaac cacgaagagc gcaccacaaa 360  
 caccaaagga gccggcccct acgactccta aggaacccaa accggcacca accactccgg 420  
 a 421

<210> 21  
 <211> 139  
 <212> PRT  
 <213> Artificial

<220>

<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15
Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro  
 50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro  
 65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr  
 85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr  
 100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 115 120 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro  
 130 135

&lt;210&gt; 22

&lt;211&gt; 3303

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Recombinant PRG4-Lub:5 cDNA construct

&lt;400&gt; 22

atggcatgga aaacacttcc catttacctg ttgttgcctg tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcaggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgcctg ccctgatttc 180

aagagagtct gcaactgcga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgcctg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcaagctgt aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc 780

agaccagtc ttccacctaa ttctgatata tctaaagaga cgtctttgac agtgaataaa 840



gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900  
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960  
 ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaa 1020  
 ggccctgctc tcaccactcc caaggagccc acgcccacca ctccaagga gcctgcatct 1080  
 accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140  
 cccgcaccta ccacgacaaa gtcagctcct actacgccc aagagccagc gccgacgact 1200  
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 gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg 1500  
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 gagcctacca ctatccaaa aagccctgat gaatcaactc ctgagctttc tgcagaaccc 1740  
 acacaaaaag ctcttgaaaa cagtcccaag gaacctggtg tacctacaac taagacgccg 1800  
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 gtaactacaa caaaaaagac aattactacc actgagatta tgaacaaacc tgaagaaaca 2100  
 gctaaaccaa aagacagagc tactaattct aaagcgacaa ctctaaacc tcaaaagcca 2160  
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 acctcaagaa tagcagaagc catgctcaa accaccacca gacctaacca aactccaaac 2340  
 tccaaactag ttgaagtaaa tccaaagagt gaagatgcag gtggtgctga aggagaaaca 2400  
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 ttaccgagag tacccaatca aggcattatc atcaatccca tgctttccga tgagaccaat 2520  
 atatgcaatg gtaagccagt agatggactg actactttgc gcaatgggac attagttgca 2580  
 ttccgaggtc attatttctg gatgctaagt ccattcagtc caccatctcc agctcgcaga 2640

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attactgaag tttggggtat tccttcccc attgatactg tttttactag gtgcaactgt 2700
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gatgcagggt accccaaacc aattttcaaa ggatttggag gactaactgg acaaatagtg 2820
gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga 2880
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gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatatcc acctgccaga 3060
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tatgattact atgccttttc taaagatcaa tactataaca ttgatgtgcc tagtagaaca 3240
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<210> 23  
 <211> 1100  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Amino acid sequence of entire PRG4-LUB:5 protein.

<400> 23

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20           25           30
Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35           40           45
Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50           55           60
Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65           70           75           80
Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85           90           95
Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100          105          110
Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115          120          125

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Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys  
 130 135 140  
 Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val  
 145 150 155 160  
 Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser  
 165 170 175  
 Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg  
 180 185 190  
 Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr  
 195 200 205  
 Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser  
 210 215 220  
 Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr  
 225 230 235 240  
 Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys  
 245 250 255  
 Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys  
 260 265 270  
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu  
 275 280 285  
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr  
 290 295 300  
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp  
 305 310 315 320  
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu  
 325 330 335  
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro  
 340 345 350  
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro  
 355 360 365  
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr  
 370 375 380  
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 385 390 395 400  
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
 405 410 415  
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro  
 420 425 430  
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr

435		440		445
Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys				
450		455		460
Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys				
465		470		475
				480
Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu				
		485		490
				495
Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu				
		500		505
				510
Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro				
		515		520
				525
Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu				
		530		535
				540
Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys				
		545		550
				555
Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu				
		565		570
				575
Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro				
		580		585
				590
Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr				
		595		600
				605
Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro				
		610		615
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Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr				
		625		630
				635
				640
Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val				
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				655
Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu				
		660		665
				670
Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile				
		675		680
				685
Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys				
		690		695
				700
Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro				
		705		710
				715
				720
Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met				
		725		730
				735
Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr				
		740		745
				750

Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met  
 755 760 765  
 Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val  
 770 775 780  
 Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr  
 785 790 795 800  
 Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro  
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 Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn  
 820 825 830  
 Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp  
 835 840 845  
 Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His  
 850 855 860  
 Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg  
 865 870 875 880  
 Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr  
 885 890 895  
 Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr  
 900 905 910  
 Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile  
 915 920 925  
 Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser  
 930 935 940  
 Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg  
 945 950 955 960  
 Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys  
 965 970 975  
 Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met  
 980 985 990  
 Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln  
 995 1000 1005  
 Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr  
 1010 1015 1020  
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu  
 1025 1030 1035  
 Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro  
 1040 1045 1050  
 Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys  
 1055 1060 1065

Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala  
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Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn  
 1085 1090 1095

Cys Pro  
 1100

<210> 24  
 <211> 514  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA  
 cassette-2 sequences

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 ccaagagacc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120  
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180  
 aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240  
 ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaaag 300  
 aaccagcccc tactacgaca aaggagcctg caccacacac cacgaagagc gcacccacaa 360  
 caccaaagga gccggcccct acgactccta aagaaccagc ccctactacg acaaaggagc 420  
 ctgcacccac aaccacgaag agcgaccca caacaccaaa ggagccggcc cctacgactc 480  
 ctaaggaacc caaaccggca ccaaccactc cgga 514

<210> 25  
 <211> 170  
 <212> PRT  
 <213> Artificial

<220>  
 <223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences  
 between S373 and E544 in SEQ ID NO: 23)

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Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala  
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro  
50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro  
65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr  
85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr  
100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr  
115 120 125

Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr  
130 135 140

Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro  
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Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro  
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<210> 26

<211> 45

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "APTTTPKEPAPTTTTSAPTTPKEPAPTTT  
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protein

<400> 26

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala  
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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala  
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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys  
35 40 45

<210> 27

<211> 31

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "KEPAPTTTKEPAPTTTTSAPTTPKEPAPTTTP" (31 amino  
acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

40

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1 5 10 15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro  
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&lt;210&gt; 28

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

<223> Amino acid sequence "EPAPTTTKSAPTTTPKEPAPTTTP" (22 amino acids)  
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preferred PRG4-LUB:N protein where N = 3 or more.

&lt;400&gt; 28

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu  
1 5 10 15

Pro Ala Pro Thr Thr Pro  
20

&lt;210&gt; 29

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

<223> Amino acid sequence "KEPKPAPTTTP" (10 amino acids) in preferred  
PRG4-LUB:N protein where N = 2 or more.

&lt;400&gt; 29

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro  
1 5 10